L4 ANSWER 1 OF 1 MEDLINE
AN 96081515 MEDLINE
DN 96081515 PubMed ID: 8538493
TI A metallo-dependent **cysteine proteinase** of **Cryptosporidium** parvum associated with the surface of sporozoites.
AU Nesterenko M V; Tilley M; Upton S J
CS Division of Biology, Kansas State University, Manhattan 66506, USA.
NC AI30881 (NIAID)
SO MICROBIOS, (1995) 83 (335) 77-88.
Journal code: 0207257. ISSN: 0026-2633.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199602
ED Entered STN: 19960221
Last Updated on STN: 20000303
Entered Medline: 19960205
AB A proteinase of 24 kD was found associated with sporozoites of **Cryptosporidium** parvum. Optimal hydrolysis of azocasein, casein, bovine serum albumin, and gelatin occurred at a pH of 6.5-7.0. Activity against azocasein was inhibited by ethylenediaminotetraacetic acid (EDTA), iodoacetic acid (IAA), trans-epoxysuccinyl-L-leucylamido(4-guanido) butane (E-64), and phosphoramidon, suggesting that the enzyme was a metallo-dependent **cysteine proteinase**. Both serine and aspartate protease inhibitors failed to inhibit enzyme activity. The enzyme was partially purified by preparative isoelectric focusing of parasite membrane proteins. Polyclonal antiserum to parasite membrane proteins was generated in rats. The enzyme-containing fraction was subjected to SDS-PAGE and probed with antiserum, and the **antibodies** against the protease were eluted directly from nitrocellulose blots. An indirect immunofluorescence assay using these monospecific **antibodies** revealed that the protease occurred on the surface of sporozoites, but was not associated with oocyst walls, rhoptries, or micronemes.

(FILE 'HOME' ENTERED AT 15:55:09 ON 17 OCT 2002)

FILE 'MEDLINE' ENTERED AT 15:56:28 ON 17 OCT 2002

```
L1        618863 S ANTIBOD?
L2          3245 S CRYPTOSPORIDIUM
L3         14382 S CYSTEINE PROTEINASE# OR CATHEPSIN#
L4             1 S L1 AND L2 AND L3

=>
```

L3 ANSWER 1 OF 1 MEDLINE
AN 95359407 MEDLINE
DN 95359407 PubMed ID: 7632919
TI Ethylene-regulated expression of a **carnation cysteine proteinase during** flower petal senescence.
AU Jones M L; Larsen P B; Woodson W R
CS Department of Horticulture, Purdue University, West Lafayette, IN 47907-1165, USA.
SO PLANT MOLECULAR BIOLOGY, (1995 Jun) 28 (3) 505-12.
Journal code: 9106343. ISSN: 0167-4412.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U17135
EM 199509
ED Entered STN: 19950921
Last Updated on STN: 20000303
Entered Medline: 19950912
AB The senescence of carnation (Dianthus caryophyllus L.) flower petals is regulated by the phytohormone ethylene and is associated with considerable catabolic activity including the loss of protein. In this paper we present the molecular cloning of a cysteine proteinase and show that its expression is regulated by ethylene and associated with petal senescence. A 1600 bp cDNA was amplified by polymerase chain reaction using a 5'-specific primer and 3'-nonspecific primer designed to amplify a 1-aminocyclopropane-1-carboxylate synthase cDNA from reverse-transcribed stylar RNA. The nucleotide sequence of the cloned product (pDCCP1) was found to share significant homology to several cysteine proteinases rather than ACC synthase. A single open reading frame of 428 amino acids was shown to share significant homology with other plant cysteine proteinases including greater than 70% identity with a cysteine proteinase from Arabidopsis thaliana. Amino acids in the active site of cysteine proteinases were conserved in the pDCCP1 peptide. RNA gel blot analysis revealed that the expression of pDCCP1 increased substantially with the onset of ethylene production and senescence of petals. Increased pDCCP1 expression was also associated with ethylene production in other senescing floral organs including ovaries and styles. The pDCCP1 transcript accumulated in petals treated with exogenous ethylene within 3 h and treatment of flowers with 2,5-norbornadiene, an inhibitor of ethylene action, prevented the increase in pDCCP1 expression in petals. The temporal and spatial patterns of pDCCP1 expression suggests a role for cysteine proteinase in the loss of protein during floral senescence.

=>

```
          1291 DROUGHT
         35815 INDUCIBLE
L2           1 ENCODE DISTINCT DROUGHT INDUCIBLE
                 (ENCODE(W)DISTINCT(W)DROUGHT(W)INDUCIBLE)

=> D BIB AB

L2   ANSWER 1 OF 1     MEDLINE
AN   93314960     MEDLINE
DN   93314960   PubMed ID: 8325504
TI   Structure and expression of two genes that encode
     distinct drought-inducible cysteine
     proteinases in Arabidopsis thaliana.
AU   Koizumi M; Yamaguchi-Shinozaki K; Tsuji H; Shinozaki K
CS   Laboratory of Plant Molecular Biology, Tsukuba Life Science Center,
     Institute of Physical and Chemical Research (RIKEN), Ibaraki, Japan.
SO   GENE, (1993 Jul 30) 129 (2) 175-82.
     Journal code: 7706761. ISSN: 0378-1119.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals; Space Life Sciences
OS   GENBANK-D13042; GENBANK-D13043; GENBANK-L03653; GENBANK-L03654;
     GENBANK-L05530; GENBANK-L07632; GENBANK-M96931; GENBANK-M96932;
     GENBANK-M96933; GENBANK-X54209
EM   199308
ED   Entered STN: 19930820
     Last Updated on STN: 20010625
     Entered Medline: 19930812
AB   Among nine cDNA clones (named RD) corresponding to genes that are
     responsive to dehydration in Arabidopsis thaliana, two clones, RD19 and
     RD21, were analyzed further. Northern blot analysis revealed that both the
     RD19 and RD21 mRNAs were not induced by abscisic acid. Neither RD19 nor
     RD21 mRNA synthesis was responsive to cold or to heat stress. On the other
     hand, transcription of both the RD19 and RD21 mRNAs was strongly induced
     under high-salt conditions, which suggests that the genes corresponding to
     RD19 and RD21 may be induced by changes in the osmotic potential of plant
     cells. Putative proteins, RD19 and RD21, encoded by two of the RD cDNAs
     have amino acid (aa) sequences typical of the catalytic sites of cysteine
     proteinases (CysP). RD21 and RD19 appeared to contain signal peptides that
     function in protein secretion. RD21 contains an aa sequence similar to
     that of the C-terminal extension peptide. Phylogenetic tree analysis
     indicated that the putative RD21 and RD19 proteins are quite different
     types of CysP. Genomic Southern analysis revealed that each gene family
     contains at least two members, which do not cross-hybridize. The two genes
     corresponding to RD19 and RD21 (rd19A and rd21A, respectively) were cloned
     and their structural analysis revealed the presence of two and four
     introns, respectively. The numbers and sites of introns differ between the
     genes, supporting our hypothesis that rd19A and rd21A belong to different
     subfamilies of genes encoding CysP. The transcription start points were
     determined by primer extension. Two conserved sequences were found in the
     promoter regions of the two genes.
```

L6 ANSWER 1 OF 1 MEDLINE
AN 97094976 MEDLINE
DN 97094976 PubMed ID: 8939744
TI The **prosequence** of **procaricain** forms an alpha-helical domain that prevents access to the substrate-binding cleft.
AU Groves M R; Taylor M A; Scott M; Cummings N J; Pickersgill R W; Jenkins J A
CS Department of Food Macromolecular Science, Institute of Food Research, Reading, UK.
SO STRUCTURE, (1996 Oct 15) 4 (10) 1193-203.
Journal code: 9418985. ISSN: 0969-2126.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS PDB-1PCI; PDB-R1PCISF
EM 199701
ED Entered STN: 19970219
Last Updated on STN: 20000303
Entered Medline: 19970128
AB BACKGROUND: Cysteine proteases are involved in a variety of cellular processes including cartilage degradation in arthritis, the progression of Alzheimer's disease and cancer invasion: these enzymes are therefore of immense biological importance. Caricain is the most basic of the cysteine proteases found in the latex of Carica papaya. It is a member of the papain superfamily and is homologous to other plant and animal cysteine proteases. Caricain is naturally expressed as an inactive zymogen called procaricain. The inactive form of the protease contains an inhibitory proregion which consists of an additional 106 N-terminal amino acids; the proregion is removed upon activation. RESULTS: The crystal structure of procaricain has been refined to 3.2 A resolution; the final model consists of three non-crystallographically related molecules. The proregion of caricain forms a separate globular domain which binds to the C-terminal domain of mature caricain. The proregion also contains an extended polypeptide chain which runs through the substrate-binding cleft, in the opposite direction to that of the substrate, and connects to the N terminus of the mature region. The mature region does not undergo any conformational change on activation. CONCLUSIONS: We conclude that the rate-limiting step in the in vitro activation of procaricain is the dissociation of the prodomain, which is then followed by proteolytic cleavage of the extended polypeptide chain of the proregion. The prodomain provides a stable scaffold which may facilitate the folding of the C-terminal lobe of procaricain.

=>

L8 ANSWER 1 OF 1 MEDLINE
AN 97051808 MEDLINE
DN 97051808 PubMed ID: 8896443
TI Structure of **human procathepsin L**
reveals the molecular basis of inhibition by the prosegment.
AU Coulombe R; Grochulski P; Sivaraman J; Menard R; Mort J S; Cygler M
CS Biotechnology Research Institute, National Research Council of Canada, Montreal, Quebec.
SO EMBO JOURNAL, (1996 Oct 15) 15 (20) 5492-503.
Journal code: 8208664. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 20020420
Entered Medline: 19961206
AB Cathepsin L is a member of the papain superfamily of cysteine proteases and, like many other proteases, it is synthesized as an inactive proenzyme. Its prosegment shows little homology to that of procathepsin B, whose structure, the first for a cysteine protease proenzyme, has been determined recently. We report here the 3-D structure of a mutant of human procathepsin L determined at 2.2 A resolution, describe the mode of binding employed by the prosegment and discuss the molecular basis for other possible roles of the prosegment. The N-terminal part of the prosegment is globular and contains three alpha-helices with a small hydrophobic core built around aromatic side chains. This domain packs against a loop on the enzyme's surface, with the aromatic side chain from the prosegment being located in the center of this loop and providing a large contact area. The C-terminal portion of the prosegment assumes an extended conformation and follows along the substrate binding cleft toward the N-terminus of the mature enzyme. The direction of the prosegment in the substrate binding cleft is opposite to that of substrates. The previously described role of the prosegment in the interactions with membranes is supported by the structure of its N-terminal domain. The fold of the prosegment and the mechanism by which it inhibits the enzymatic activity of procathepsin L is similar to that observed in procathepsin B despite differences in length and sequence, suggesting that this mode of inhibition is common to all enzymes from the papain superfamily.

=>